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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/226,046DATE: 08/06/1999
TIME: 15:41:04

Input Set: I226046.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Reppert, Steven M.
 2 Ebisawa, Takashi
 3 <120> TITLE OF INVENTION: HIGH-AFFINITY MELATONIN RECEPTOR AND USES THEREOF
 4 <130> FILE REFERENCE: 10217/250003
 5 <140> CURRENT APPLICATION NUMBER: US/09/226,046
 6 <141> CURRENT FILING DATE: 1999-01-05
 7 <150> EARLIER APPLICATION NUMBER: US 08/466,103
 8 <151> EARLIER FILING DATE: 1995-06-06
 9 <150> EARLIER APPLICATION NUMBER: US 08/319,887
 10 <151> EARLIER FILING DATE: 1994-10-07
 11 <150> EARLIER APPLICATION NUMBER: US 08/261,857
 12 <151> EARLIER FILING DATE: 1994-06-17
 13 <160> NUMBER OF SEQ ID NOS: 29
 14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 15 <210> SEQ ID NO 1
 16 <211> LENGTH: 1320
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Xenopus laevis
 19 <220> FEATURE:
 20 <221> NAME/KEY: CDS
 21 <222> LOCATION: (32)...(1291)
 22 <400> SEQUENCE: 1

23	tgcctatctc ccttgccag gggcagaga a atg atg gag gtg aat agc act	52
24	Met Met Glu Val Asn Ser Thr	
25	1 5	
26	tgc ttg gat tgc agg aca cct ggt acc ata cga aca gag cag gat gca	100
27	Cys Leu Asp Cys Arg Thr Pro Gly Thr Ile Arg Thr Glu Gln Asp Ala	
28	10 15 20	
29	cag gac agc gca tct cag gga ctc acc tct gcc ctg gcg gtg gtt ctt	148
30	Gln Asp Ser Ala Ser Gln Gly Leu Thr Ser Ala Leu Ala Val Val Leu	
31	25 30 35	
32	ata ttc acc att gtt gtg gat gtc ctg ggc aat ata ttg gtc att ttg	196
33	Ile Phe Thr Ile Val Val Asp Val Leu Gly Asn Ile Leu Val Ile Leu	
34	40 45 50 55	
35	tct gtc ctg agg aac aag aag ctg cag aat gct gga aat ctc ttt gtt	244
36	Ser Val Leu Arg Asn Lys Lys Leu Gln Asn Ala Gly Asn Leu Phe Val	
37	60 65 70	
38	gtc agt ttg tct att gcc gat ctg gtt gct gtg tat ccc tat ccg	292
39	Val Ser Leu Ser Ile Ala Asp Leu Val Val Ala Val Tyr Pro Tyr Pro	
40	75 80 85	
41	gtc att ctc ata gct att ttc cag aat gga tgg acg ctt gga aat atc	340
42	Val Ile Leu Ile Ala Ile Phe Gln Asn Gly Trp Thr Leu Gly Asn Ile	
43	90 95 100	
44	cat tgt cag atc agt ggc ttc ctg atg gga ctc agc gtt att gga tca	388

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45	His Cys Gln Ile Ser Gly Phe Leu Met Gly Leu Ser Val Ile Gly Ser				
46	105	110	115		
47	gtc ttc aac ata aca gcc ata gct atc aac agg tat tgc tac atc tgc			436	
48	Val Phe Asn Ile Thr Ala Ile Ala Ile Asn Arg Tyr Cys Tyr Ile Cys				
49	120	125	130	135	
50	cac agc ctg aga tat gac aag ctt tat aat caa aga agc acc tgg tgc			484	
51	His Ser Leu Arg Tyr Asp Lys Leu Tyr Asn Gln Arg Ser Thr Trp Cys				
52	140	145	150		
53	tac ctt ggc ctg aca tgg ata cta act ata att gca atc gtg cca aac			532	
54	Tyr Leu Gly Leu Thr Trp Ile Leu Thr Ile Ile Ala Ile Val Pro Asn				
55	155	160	165		
56	ttt ttt gtt gga tca cta cag tat gac ccc agg att ttt tct tgc aca			580	
57	Phe Phe Val Gly Ser Leu Gln Tyr Asp Pro Arg Ile Phe Ser Cys Thr				
58	170	175	180		
59	ttt gcg cag aca gtg agt tcc tca tac acc ata aca gta gtg gtg gtg			628	
60	Phe Ala Gln Thr Val Ser Ser Tyr Thr Ile Thr Val Val Val Val				
61	185	190	195		
62	cat ttt ata gtc cct ctt agt gtt gtg aca ttc tgt tac tta aga ata			676	
63	His Phe Ile Val Pro Leu Ser Val Val Thr Phe Cys Tyr Leu Arg Ile				
64	200	205	210	215	
65	tgg gtt tta gtg atc caa gtc aaa cac aga gtt aga caa gac ttc aag			724	
66	Trp Val Leu Val Ile Gln Val Lys His Arg Val Arg Gln Asp Phe Lys				
67	220	225	230		
68	caa aag ttg aca caa aca gac ttg aga aat ttc ttg acc atg ttt gtg			772	
69	Gln Lys Leu Thr Gln Thr Asp Leu Arg Asn Phe Leu Thr Met Phe Val				
70	235	240	245		
71	gtc ttt gta ctt ttt gca gtt tgc tgg gcc ccc tta aac ttt atc ggc			820	
72	Val Phe Val Phe Ala Val Cys Trp Ala Pro Leu Asn Phe Ile Gly				
73	250	255	260		
74	ctt gct gtg gcc att aat ccg ttt cat gtg gca cca aag att cca gaa			868	
75	Leu Ala Val Ala Ile Asn Pro Phe His Val Ala Pro Lys Ile Pro Glu				
76	265	270	275		
77	tgg ctg ttt gtt tta agc tat ttc atg gcc tat ttt aac agt tgt ctc			916	
78	Trp Leu Phe Val Leu Ser Tyr Phe Met Ala Tyr Phe Asn Ser Cys Leu				
79	280	285	290	295	
80	aat gct gtt ata tat ggt gtg cta aat caa aac ttc cgc aag gag tac			964	
81	Asn Ala Val Ile Tyr Gly Val Leu Asn Gln Asn Phe Arg Lys Glu Tyr				
82	300	305	310		
83	aaa aga ata ctg atg tcc tta ttg act cca aga ctg ttg ttt ctt gac			1012	
84	Lys Arg Ile Leu Met Ser Leu Leu Thr Pro Arg Leu Leu Phe Leu Asp				
85	315	320	325		
86	aca tct aga gga gga act gag gga ttg aaa agt aag cct tcg cca gct			1060	
87	Thr Ser Arg Gly Gly Thr Glu Gly Leu Lys Ser Lys Pro Ser Pro Ala				
88	330	335	340		
89	gta acc aac aac aat caa gca gat atg cta gga gaa gca agg tca ctg			1108	
90	Val Thr Asn Asn Asn Gln Ala Asp Met Leu Gly Glu Ala Arg Ser Leu				
91	345	350	355		
92	tgg ctg agc agg aga aat ggt gcg aaa atg gtg atc atc atc agg cca			1156	
93	Trp Leu Ser Arg Arg Asn Gly Ala Lys Met Val Ile Ile Arg Pro				
94	360	365	370	375	

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95 aga aaa gca caa att gca atc atc cat caa ata ttc tgg cct cag agt 1204
 96 Arg Lys Ala Gln Ile Ala Ile Ile His Gln Ile Phe Trp Pro Gln Ser
 97 380 385 390
 98 tca tgg gca aca tgc cgt caa gac aca aag att acc gga gaa gaa gat 1252
 99 Ser Trp Ala Thr Cys Arg Gln Asp Thr Lys Ile Thr Gly Glu Glu Asp
 100 395 400 405
 101 ggc tgc cgt gaa ctg tgc aag gac ggg att tcc caa agg tgagaccaa 1301
 102 Gly Cys Arg Glu Leu Cys Lys Asp Gly Ile Ser Gln Arg
 103 410 415 420
 104 tgcactatat ccacattat 1320
 105 <210> SEQ ID NO 2
 106 <211> LENGTH: 420
 107 <212> TYPE: PRT
 108 <213> ORGANISM: Xenopus laevis
 109 <400> SEQUENCE: 2
 110 Met Met Glu Val Asn Ser Thr Cys Leu Asp Cys Arg Thr Pro Gly Thr
 111 1 5 10 15
 112 Ile Arg Thr Glu Gln Asp Ala Gln Asp Ser Ala Ser Gln Gly Leu Thr
 113 20 25 30
 114 Ser Ala Leu Ala Val Val Leu Ile Phe Thr Ile Val Val Asp Val Leu
 115 35 40 45
 116 Gly Asn Ile Leu Val Ile Leu Ser Val Leu Arg Asn Lys Lys Leu Gln
 117 50 55 60
 118 Asn Ala Gly Asn Leu Phe Val Val Ser Leu Ser Ile Ala Asp Leu Val
 119 65 70 75 80
 120 Val Ala Val Tyr Pro Tyr Pro Val Ile Leu Ile Ala Ile Phe Gln Asn
 121 85 90 95
 122 Gly Trp Thr Leu Gly Asn Ile His Cys Gln Ile Ser Gly Phe Leu Met
 123 100 105 110
 124 Gly Leu Ser Val Ile Gly Ser Val Phe Asn Ile Thr Ala Ile Ala Ile
 125 115 120 125
 126 Asn Arg Tyr Cys Tyr Ile Cys His Ser Leu Arg Tyr Asp Lys Leu Tyr
 127 130 135 140
 128 Asn Gln Arg Ser Thr Trp Cys Tyr Leu Gly Leu Thr Trp Ile Leu Thr
 129 145 150 155 160
 130 Ile Ile Ala Ile Val Pro Asn Phe Phe Val Gly Ser Leu Gln Tyr Asp
 131 165 170 175
 132 Pro Arg Ile Phe Ser Cys Thr Phe Ala Gln Thr Val Ser Ser Tyr
 133 180 185 190
 134 Thr Ile Thr Val Val Val His Phe Ile Val Pro Leu Ser Val Val
 135 195 200 205
 136 Thr Phe Cys Tyr Leu Arg Ile Trp Val Leu Val Ile Gln Val Lys His
 137 210 215 220
 138 Arg Val Arg Gln Asp Phe Lys Gln Lys Leu Thr Gln Thr Asp Leu Arg
 139 225 230 235 240
 140 Asn Phe Leu Thr Met Phe Val Val Phe Val Leu Phe Ala Val Cys Trp
 141 245 250 255
 142 Ala Pro Leu Asn Phe Ile Gly Leu Ala Val Ala Ile Asn Pro Phe His
 143 260 265 270
 144 Val Ala Pro Lys Ile Pro Glu Trp Leu Phe Val Leu Ser Tyr Phe Met

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Input Set: I226046.RAW

145 275 280 285
 146 Ala Tyr Phe Asn Ser Cys Leu Asn Ala Val Ile Tyr Gly Val Leu Asn
 147 290 295 300
 148 Gln Asn Phe Arg Lys Glu Tyr Lys Arg Ile Leu Met Ser Leu Leu Thr
 149 305 310 315 320
 150 Pro Arg Leu Leu Phe Leu Asp Thr Ser Arg Gly Gly Thr Glu Gly Leu
 151 325 330 335
 152 Lys Ser Lys Pro Ser Pro Ala Val Thr Asn Asn Asn Gln Ala Asp Met
 153 340 345 350
 154 Leu Gly Glu Ala Arg Ser Leu Trp Leu Ser Arg Arg Asn Gly Ala Lys
 155 355 360 365
 156 Met Val Ile Ile Ile Arg Pro Arg Lys Ala Gln Ile Ala Ile Ile His
 157 370 375 380
 158 Gln Ile Phe Trp Pro Gln Ser Ser Trp Ala Thr Cys Arg Gln Asp Thr
 159 385 390 395 400
 160 Lys Ile Thr Gly Glu Asp Gly Cys Arg Glu Leu Cys Lys Asp Gly
 161 405 410 415
 162 Ile Ser Gln Arg
 163 420
 164 <210> SEQ ID NO 3
 165 <211> LENGTH: 1149
 166 <212> TYPE: DNA
 167 <213> ORGANISM: Ovis
 168 <220> FEATURE:
 169 <221> NAME/KEY: CDS
 170 <222> LOCATION: (49)...(1146)
 171 <400> SEQUENCE: 3
 172 gggagctcga cgctctgggg atccaccggc gccggccctg ccagcgcg atg gcg ggg 57
 173 Met Ala Gly
 174 1
 175 cgg ctg tgg ggc tcg ccg ggc ggg acc ccc aag ggc aac ggc agc agc 105
 176 Arg Leu Trp Gly Ser Pro Gly Gly Thr Pro Lys Gly Asn Gly Ser Ser
 177 5 10 15
 178 gcg ctg ctc aac gtc tcg cag gcg ccc ggc gac ggt gtg 153
 179 Ala Leu Leu Asn Val Ser Gln Ala Ala Pro Gly Ala Gly Asp Gly Val
 180 20 25 30 35
 181 cgg ccg cgg ccc tcg tgg ctg gcc acc ctc gcc tcc atc ctc atc 201
 182 Arg Pro Arg Pro Ser Trp Leu Ala Ala Thr Leu Ala Ser Ile Leu Ile
 183 40 45 50
 184 ttc acc atc gtg gac atc gtg ggc aac ctc ctg gtg gtc ctg tcc 249
 185 Phe Thr Ile Val Val Asp Ile Val Gly Asn Leu Leu Val Val Leu Ser
 186 55 60 65
 187 gtg tat cgg aac aag aag ctg agg aac gca ggg aat gtg ttt gtg gtg 297
 188 Val Tyr Arg Asn Lys Lys Leu Arg Asn Ala Gly Asn Val Phe Val Val
 189 70 75 80
 190 agc ctg gca gtt gca gac ctg ctg gtg gcc gtg tat ccg tac ccc ttg 345
 191 Ser Leu Ala Val Ala Asp Leu Leu Val Ala Val Tyr Pro Tyr Pro Leu
 192 85 90 95
 193 gcg ctg gcg tct ata gtt aac aat ggg tgg agc ctg agc tcc ctg cat 393
 194 Ala Leu Ala Ser Ile Val Asn Asn Gly Trp Ser Leu Ser Ser Leu His

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RAW SEQUENCE LISTING
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195	100	105	110	115
196	tgc caa ctt agt ggc ttc ctg atg ggc ttg agc gtc atc ggg tcc gtt			441
197	Cys Gln Leu Ser Gly Phe Leu Met Gly Leu Ser Val Ile Gly Ser Val			
198	120	125	130	
199	ttc agc atc acg gga att gcc atc aac cgc tat tgc tgc atc tgc cac			489
200	Phe Ser Ile Thr Gly Ile Ala Ile Asn Arg Tyr Cys Cys Ile Cys His			
201	135	140	145	
202	agc ctc aga tac ggc aag ctg tat agc ggc acg aat tcc ctc tgc tac			537
203	Ser Leu Arg Tyr Gly Lys Leu Tyr Ser Gly Thr Asn Ser Leu Cys Tyr			
204	150	155	160	
205	gtg ttc ctg atc tgg acg ctg acg ctc gtg gcg atc gtg ccc aac ctg			585
206	Val Phe Leu Ile Trp Thr Leu Thr Leu Val Ala Ile Val Pro Asn Leu			
207	165	170	175	
208	tgt gtg ggg acc ctg cag tac gac ccg agg atc tat tcc tgt acc ttc			633
209	Cys Val Gly Thr Leu Gln Tyr Asp Pro Arg Ile Tyr Ser Cys Thr Phe			
210	180	185	190	195
211	acg cag tcc gtc agc tca gcc tac acg atc gcc gtg gtg ttc cat			681
212	Thr Gln Ser Val Ser Ser Ala Tyr Thr Ile Ala Val Val Val Phe His			
213	200	205	210	
214	ttc ata gtt ccg atg ctc gta gtc gtc ttc tgt tac ctg aga atc tgg			729
215	Phe Ile Val Pro Met Leu Val Val Phe Cys Tyr Leu Arg Ile Trp			
216	215	220	225	
217	gcc ctg gtt ctt cag gtc aga tgg aag gtg aaa ccg gac aac aaa ccg			777
218	Ala Leu Val Leu Gln Val Arg Trp Lys Val Lys Pro Asp Asn Lys Pro			
219	230	235	240	
220	aaa ctg aag ccc cag gac ttc agg aat ttt gtc acc atg ttt gtg gtt			825
221	Lys Leu Lys Pro Gln Asp Phe Arg Asn Phe Val Thr Met Phe Val Val			
222	245	250	255	
223	ttt gtc ctc ttt gcc att tgc tgg gct cct ctg aac ttc att ggt ctc			873
224	Phe Val Leu Phe Ala Ile Cys Trp Ala Pro Leu Asn Phe Ile Gly Leu			
225	260	265	270	275
226	gtt gtg gcc tcg gac ccc gcc agc atg gca ccc agg atc ccc gag tgg			921
227	Val Val Ala Ser Asp Pro Ala Ser Met Ala Pro Arg Ile Pro Glu Trp			
228	280	285	290	
229	ctg ttt gtg gct agt tac tat atg gca tat ttc aac agc tgc ctc aat			969
230	Leu Phe Val Ala Ser Tyr Tyr Met Ala Tyr Phe Asn Ser Cys Leu Asn			
231	295	300	305	
232	gcg atc ata tat gga cta ctg aac caa aat ttc agg cag gaa tac aga			1017
233	Ala Ile Tyr Gly Leu Leu Asn Gln Asn Phe Arg Gln Glu Tyr Arg			
234	310	315	320	
235	aaa att ata gtc tca ttg tgt acc acc aag atg ttc ttt gtg gat agc			1065
236	Lys Ile Ile Val Ser Leu Cys Thr Thr Lys Met Phe Phe Val Asp Ser			
237	325	330	335	
238	tcc aat cat gta gca gat aga att aaa cgc aaa ccc tct cca tta ata			1113
239	Ser Asn His Val Ala Asp Arg Ile Lys Arg Lys Pro Ser Pro Leu Ile			
240	340	345	350	355
241	gcc aac cat aac cta ata aag gtg gac tcc gtt taa			
242	Ala Asn His Asn Leu Ile Lys Val Asp Ser Val			
243	360	365		
244	<210> SEQ ID NO 4			

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I226046.RAW

Line ? Error/Warning

Original Text

408 W "N" or "Xaa" used: Feature required
433 W "N" or "Xaa" used: Feature required
824 W "N" or "Xaa" used: Feature required

Asn Pro Xaa Xaa Tyr
Gly Asn Xaa Phe Val Val
Asn Ala Xaa Xaa Tyr